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Morphological description and phylogenetic estimation of *Favolus roseus* (Polyporaceae): first documented records for the Indian mycobiota

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Abstract

During the course of macrofungal forays, we collected several wood-rotting fungi from three states in India: Bihar, Jharkhand, and Maharashtra. We identified some of these macrofungal collections as *Favolus roseus* Lloyd. A critical literature survey and taxonomic investigation established that this is the first report of *F. roseus* from India. We give a detailed morphological description, illustration, and molecular phylogeny of the species, along with taxonomic note and extended biogeographical distributional map.

Keywords

Distribution, new records, phylogenetic inference, species complex, taxonomy

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Introduction

The generic epithet *Favolus* P. Beauv. was first used by Palisot de Beauvois (1805) for a single species, *F. hirsutus* P. Beauv., which was originally collected in Africa and had a characteristic honeycomb-like hymenophore. During the taxonomic history of *Favolus* (Corner 1984; Ryvarden 1991; Núñez and Ryvarden 1995, 2001; Ryvarden and Iturriaga 2004; Silveira and Wright 2005; Drechsler-Santos et al. 2008), it had several times been considered to be synonym of *Polyporus* P. Micheli ex Adans. due to overlapping morphological attributes. One such remarkable taxon is *Polyporus tenuiculus* P. Beauv., which is morphologically highly variable; its gradual collection and characterization from North America, China, and Europe has lead to the realization that it is a species

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complex (Núñez and Ryvarden 1995, 2001). Using a molecular phylogenic approach, this complex has been demystified into three species, namely *F. brasiliensis* (Fr.) Fr., *F. roseus* Lloyd, and *F. spatulatus* (Jungh.) Lév. (Sotome et al. 2013). However, the validity of *F. tenuiculus* is questioned due to inaccessibility of its type specimen (Sotome et al. 2013). Sotome et al. (2013) revisited the taxonomic complexity of the genera *Polyporus* and *Favolus* and re-shuffled many species-level taxa based on morphology and molecular phylogeny. They defined *Favolus* as having laterally stipitate basidiomata, radially striate pileus, and non-crustose stipe surface macro-morphologically, while in sister genus *Neofavolus* Sotome & T. Hatt., there is a micro-morphologically absence of any distinct cuticle. The monophyletic nature of the genus *Favolus* is now widely supported by multigene phylogenetic studies based on materials from several regions around the world (Zhao and Cui 2017; Xing et al. 2020; Palacio et al. 2021).

Within the genus *Favolus*, the relatively small basidiomata with a grayish-orange to yellowish-orange pileus surface and large radially elongated pores makes *F. roseus* distinct from other species (Sotome et. al. 2013). So far materials for taxonomic study have been reported from Sri Lanka, Malaysia, and Singapore in Asia (Sotome et. al. 2013) and Tanzania in Africa (Juma et al. 2016). Indian species of *Favolus* are mostly based on morphological characters (Bakshi 1971; Bilgrami et al. 1991; Roy and De 1996; Leelavathy and Ganesh 2000; Mohanan 2011; Sharma 2012) and many of them are lacking phylogenetic data for comparison with other counterparts. During our study of poroid wood-rotting macro-fungi from tropical India, we have collected many interesting specimens of *Favolus* from three states: Maharashtra (Deccan Plateau); Bihar (Terai region), and Jharkhand (Rajmahal Hills). Critical macro- and micro-morphology characterization, coupled with combined nrITS and nrLSU-based phylogenetic studies (Fig. 1), revealed these specimens to be *F. roseus*, a species that has never been reported from India. Here, we report *F. roseus* for the first time from India and provide a detailed morphological description and a phylogenetic estimation using combined nrITS + nrLSU genes.

Methods

Representative survey sites included areas in the Indian states of Bihar, Jharkhand, and Maharashtra where collections of fruiting bodies/basidiomata were made by MEH, GV, and AVK during August to October from 2013 to 2019. Geographic coordinates were recorded using a Garmin e-trax30 hand-held GPS receiver. Fresh specimens were macromorphologically characterized, including nature of the host, in the field and their color was noted using the *Methuen Handbook of Colour* (Kornerup and Wanscher 1978) as a guide. The specimens were dried under hot air (50–60 °C) using room heater. Dried specimens were separated into two parts for molecular and micromorphological characterization, and kept in brown paper packets sealed in an air-tight polybag to avoid moisture and insect attack. Thin sections were randomly cut from tubes, context, and pilear surfaces covering the margin to central and basal regions of the basidiocarps using sharp blades. A 10% KOH solution was used to soften tissues, and lactophenol cotton blue and phloxine were used for staining. Melzer's reagent was chosen for testing the amyloidy of basidiospores and hyphae. Micromorphological observations, measurements, drawings and photography were done under an Olympus CX41 light microscope equipped with a 100× objective (oil immersion), drawing tube, and photographic attachments. All specimens were deposited at Central National Herbarium (CAL). The distributional map (Fig. 2) was produced in Arc GIS v. 10.5 (licensed to BSI, CNH, Howrah).

DNA extraction, PCR amplification and sequencing. Genomic DNA was extracted from 100 mg of dried basidiomes with the InstaGeneTM Matrix Genomic DNA isolation kit (Biorad, USA) following the manufacturer's instructions. The nrITS and nrLSU gene regions were amplified with primer pairs ITS-1F and ITS-4R (White et al. 1990) and LR0R and LR7 (Vilgalys and Hester 1990), respectively. PCR amplification was performed on a thermal cycler (Eppendorf, Germany) programmed for 2 min at 94 °C, followed by 35 cycles of 45 sec at 94 °C, 1 min at 55 °C, 1 min at 72 °C, and a final extension of 10 min at 72 °C. The PCR products were purified using the QIAquick PCR Purification Kit (QIAGEN, Germany). Both strands of the PCR fragment were sequenced on the 3730xl DNA Analyzer (Applied Biosystems, USA) using the amplifying primers. The sequence quality was checked using Sequence Scanner Software v. 1 (Applied Biosystems). Sequence alignment and required editing of the obtained sequences were carried out using Geneious v. 5.1 (Drummond et al. 2010). All sequences newly generated in this study were submitted to GenBank. Accession numbers of species used in the phylogenetic analysis are listed in the Table 1.

Sequence alignment and phylogenetic analysis. The nrITS and nrLSU sequences of *Favolus*, *Neofavolus*, *Polyporus*, and outgroups were acquired from a Blast search (Altschul et al. 1997), GenBank (Clark et al. 2016), and relevant literature (Sotome et al. 2013; Papp and Dima 2017; Zhou and Cui 2017). The nrITS and nrLSU sequences were initially aligned with MAFFT v. 7 (Katoh et al. 2019) using default settings and manually edited with MEGA v. 7 (Kumar et al. 2016). Two single-locus datasets were concatenated into one multi-loci dataset using BioEdit v. 7.0.9 (Hall 1999). The multi-locus dataset was phylogenetically analyzed using the maximum likelihood (ML) method. A ML phylogenetic analysis was carried out using in raxmlGUI v. 2.0 (Edler et al. 2021) with the GTRGAMMA substitution model. A maximum likelihood bootstrap (MLB) analysis with 1,000 replicates was performed using sequences

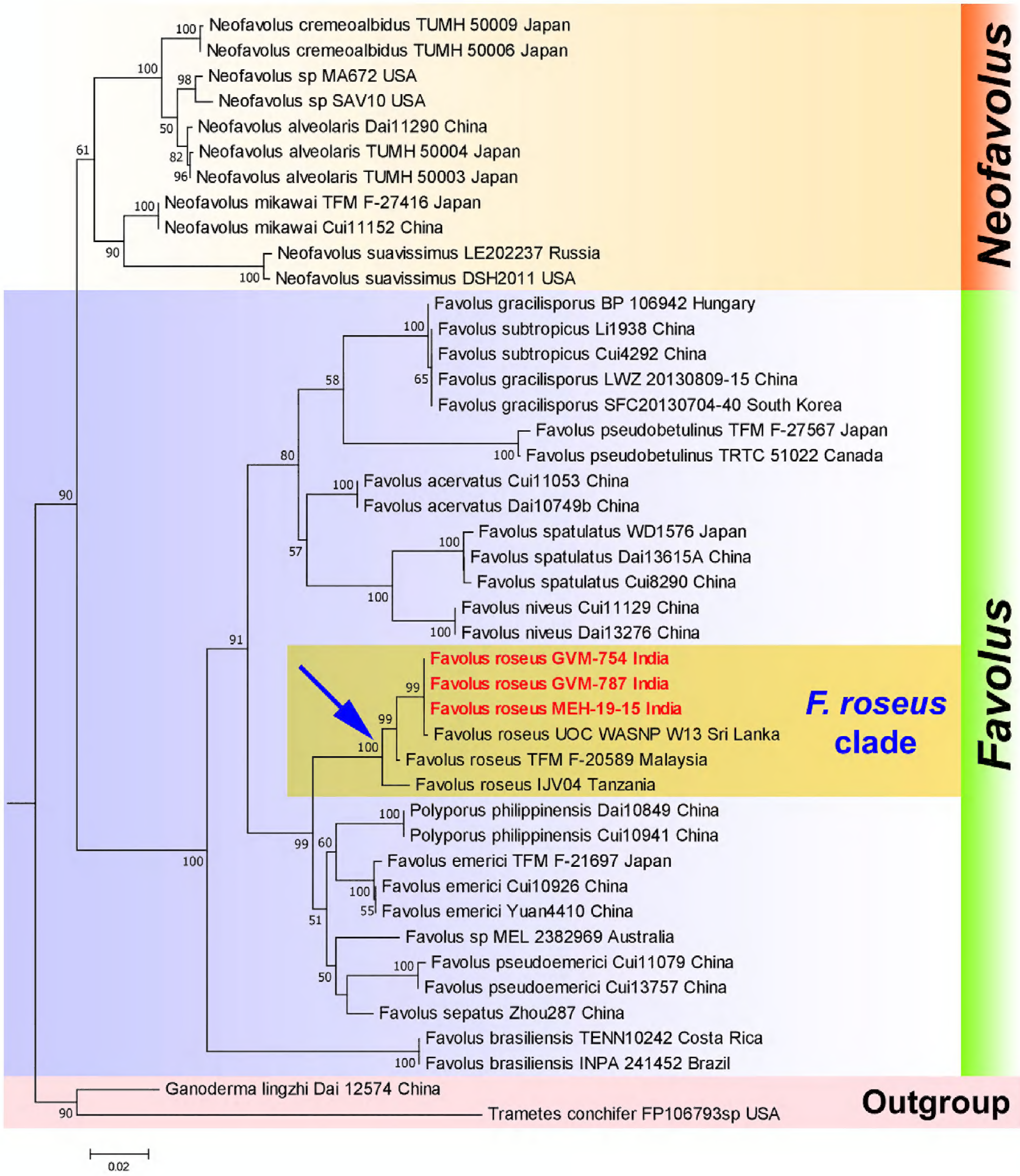
Neofavolus cremeoalbidus TUMH 50009 Japan
Neofavolus cremeoalbidus TUMH 50006 Japan
Neofavolus sp MA672 USA
Neofavolus sp SAV10 USA
Neofavolus alveolaris Dai11290 China
Neofavolus alveolaris TUMH 50004 Japan
Neofavolus alveolaris TUMH 50003 Japan
Neofavolus mikawai TFM F-27416 Japan
Neofavolus mikawai Cui11152 China
Neofavolus suavissimus LE202237 Russia
Neofavolus suavissimus DSH2011 USA
Neofavolus
Favolus gracilisporus BP 106942 Hungary
Favolus subtropicus Li1938 China
Favolus subtropicus Cui4292 China
Favolus gracilisporus LWZ 20130809-15 China
Favolus gracilisporus SFC20130704-40 South Korea
Favolus pseudobetulinus TFM F-27567 Japan
Favolus pseudobetulinus TRTC 51022 Canada
Favolus acervatus Cui11053 China
Favolus acervatus Dai10749b China
Favolus spatulatus WD1576 Japan
Favolus spatulatus Dai13615A China
Favolus spatulatus Cui8290 China
Favolus niveus Cui11129 China
Favolus niveus Dai13276 China
Favolus roseus GVM-754 India
Favolus roseus GVM-787 India
Favolus roseus MEH-19-15 India
Favolus roseus UOC WASNP W13 Sri Lanka
Favolus roseus TFM F-20589 Malaysia
Favolus roseus IJV04 Tanzania
F. roseus clade
Polyporus philippinensis Dai10849 China
Polyporus philippinensis Cui10941 China
Favolus emerici TFM F-21697 Japan
Favolus emerici Cui10926 China
Favolus emerici Yuan4410 China
Favolus sp MEL 2382969 Australia
Favolus pseudoemerici Cui11079 China
Favolus pseudoemerici Cui13757 China
Favolus sepatus Zhou287 China
Favolus brasiliensis TENN10242 Costa Rica
Favolus brasiliensis INPA 241452 Brazil
Favolus
Ganoderma lingzhi Dai 12574 China
Trametes conchifer FP106793sp USA
Outgroup
0.02

Figure 1. A maximum likelihood (ML) phylogram inferred from raxmlGUI v. 2.0 on a concatenated dataset of nrITS and nrLSU sequence data of *Favolus* and *Neofavolus* species. Bootstrap support values (≥50%) obtained from ML analysis are shown above or below the branches at nodes. Three collections of our Indian *Favolus roseus* species are shown in red and bold font in the phylogram.

of *Ganoderma lingzhi* Sheng H. Wu, Y. Cao & Y.C. Dai and *Trametes conchifer* (Schwein.) Pilát as outgroups. MLB of ≥50% and above was considered significant support for clades.

Results

Favolus roseus **Lloyd**, *Mycol. Writ.* **7**(Letter 67): 1157. (Lloyd 1922)
Figures 3, 4

Material examined. INDIA – **Maharashtra** • Marathwada, Aurangabad district, Taluka Kannad, Puranwadi; 20°22′02″N, 075°11′47″E; alt. 718 m; on logs of *Mangifera indica* L.; 17.VIII.2014; Gore Vijay (GVU/MVP-26) • Marathwada, Aurangabad district, Taluka Kannad, Nevpur; 20°23′03″N, 075°20′06″E; alt. 655 m; on logs of *M. indica*; 12.IX.2014; Gore Vijay (GVU/MVP-113) • Marathwada, Aurangabad district, Taluka Kannad, Barkatpur; 20°22′30″N, 075°23′29″E; alt. 640 m; on living

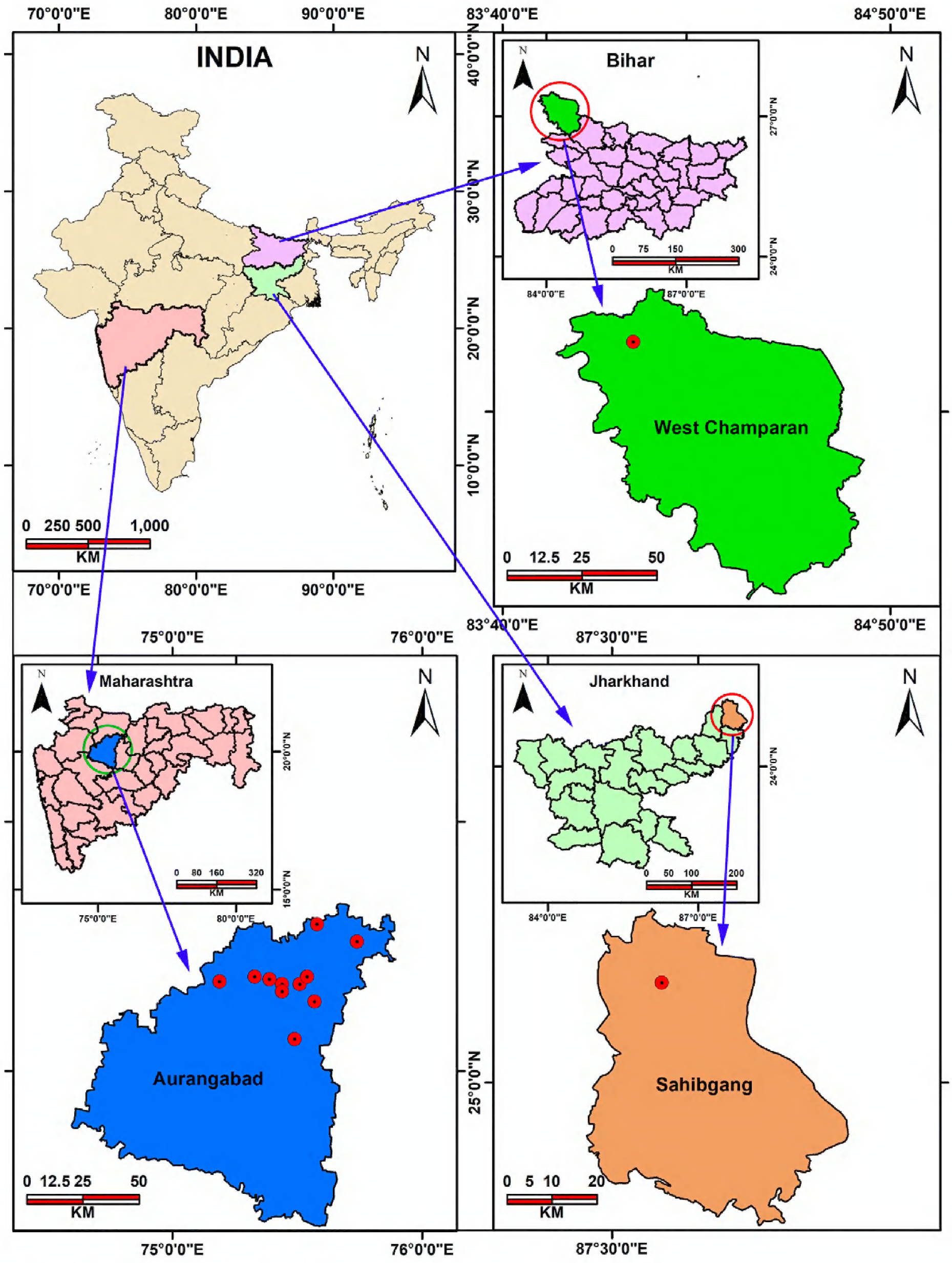

Figure 2. Distributional map of *Favolus roseus* in India.

tree of *Zizyphus mauritiana* Lam.; 29.VII.2016; Gore Vijay (GVU/MVP-209) • Marathwada, Aurangabad district, Taluka Kannad, Digoan; 20°21′03″N, 075°26′57″E; alt. 630 m; on living *Senna siamea* (Lam.) H.S. Irwin & Barneby; 08.VIII.2016; Gore Vijay (GVU/MVP-243) • Marathwada, Aurangabad district, Taluka Kannad, Aadgoan; 20°19′30″N, 075°26′41″E; alt. 650 m; on the wood logs of *M. indica*; 08.X.2016; Gore Vijay (GVU/MVP-512) • Marathwada, Aurangabad district, Taluka Phulambri, Pharshi phata; 20°08′16″N, 075°29′40″E; alt. 616 m; on the wood logs of *M. indica*; 04.X.2016; Gore Vijay (GVU/MVP-455) • Marathwada, Aurangabad

Table 1. A list of species, voucher no., GenBank accession no. and reference of species used in this study.

Species name	Voucher no.	GenBank accession no.		Reference
		ITS	nrLSU	
Favolus acervatus	Cui11053	KU189774	KU189805	Zhou and Cui 2017
F. acervatus	Dai10749b	KX548953	—	Zhou and Cui 2017
F. brasiliensis	INPA241452	AB735977	AB735953	Zhou and Cui 2017
F. brasiliensis	TENN10242	AB735976	AB368097	Zhou and Cui 2017
F. emerici	Cui10926	KU189776	KU189807	Zhou and Cui 2017
F. emerici	Yuan 4410	KX548954	—	Zhou and Cui 2017
F. emerici	TFM F-21697	AB735972	AB735951	Sotome et al. 2017
F. gracilisporus	BP 106942	MF401551	—	Papp and Dima 2017
F. gracilisporus	LWZ 20130809-15	KM385429	—	Papp and Dima 2017
F. gracilisporus	SFC20130704-40	KY038472	—	Papp and Dima 2017
F. niveus	Cui11129	KX548955	—	Zhou and Cui 2017
F. niveus	Dai13276	KX548956	—	Zhou and Cui 2017
F. philippinensis	Cui10941	KX548976	—	Zhou and Cui 2017
F. philippinensis	Dai10849	KX548978	—	Papp and Dima 2017
F. pseudobetulinus	TRTC 51022	AB587629	AB587620	Zhou and Cui 2017
F. pseudobetulinus	TFM F-27567	AB587644	AB587639	Zhou and Cui 2017
F. pseudoemerici	Cui11079	KX548958	—	Zhou and Cui 2017
F. pseudoemerici	Cui13757	KX548959	—	Zhou and Cui 2017
F. roseus	IJV04	KM593876	—	Juma et al. 2016; Papp and Dima 2017
F. roseus	TFM F-20589	AB735975	AB368099	Sotome et al. 2017
F. roseus	UOC WASNP W13	KR049231	—	Papp and Dima 2017
F. roseus	GVM-754	MT012095	MT012097	In this study
F. roseus	GVM-787	MT012371	MT012370	In this study
F. roseus	MEH-19-15	MT012096	MT012099	In this study
F. septatus	Zhou287	KX548968	—	Zhou and Cui 2017
F. spatulatus	Cui8290	KX548969	—	Zhou and Cui 2017
F. spatulatus	Dai13615A	KU189775	KU189806	Zhou and Cui 2017
F. spatulatus	WD1576	AB587633	AB587622	Sotome et al. 2013
F. subtropicus	Cui4292	KX548970	—	Zhou and Cui 2017
F. subtropicus	Li1938	KX548971	—	Zhou and Cui 2017
F. sp.	MEL2382969	KP012829	KP012829	Zhou and Cui 2017
Neofavolus alveolaris	Dai11290	KU189768	KU189799	Zhou and Cui 2017
N. alveolaris	TUMH 50003	AB735968	AB735949	Sotome et al. 2013
N. alveolaris	TUMH 50004	AB735967	AB735948	Sotome et al. 2013
N. cremeoalbidus	TUMH 50006	AB735979	AB735956	Sotome et al. 2013
N. cremeoalbidus	TUMH 50009	AB735980	AB735957	Sotome et al. 2013
N. mikawae	Cui11152	KU189773	KU189804	Zhou and Cui 2017
N. mikawae	TFM F-27416	AB735962	AB735942	Sotome et al. 2013
N. suavissimus	DSH2011	KP283496	KP283525	Zhou and Cui 2017
N. suavissimus	LE202237	KM411460	KM411476	Zhou and Cui 2017
N. sp.	MA672	KP283506	KP283524	Zhou and Cui 2017
N. sp.	SAV10	KP283507	KP283526	Zhou and Cui 2017
Trametes conchifer	FP 106793sp	JN164924	—	Zhou and Cui 2017
Ganoderma lingzhi	Dai 12574	KJ143908	—	Zhou and Cui 2017

district, Taluka Sillod, Ajanta; 20°31′14″N, 075°44′47″E; alt. 583 m; on living, main tree trunk of *Ficus benghalensis* L.; 16.VII.2016; Gore Vijay (GVU/MVP-204) • Marathwada, Aurangabad district, Taluka Sillod, Kalewadi; 20°21′28″N, 075°30′40″E; alt. 623 m; on living, main tree trunk of *F. benghalensis*; 04.VIII.2016; Gore Vijay (GVU/MVP-227) • Marathwada, Aurangabad district, Taluka Sillod, Kasod; 20°23′11″N, 075°32′28″E; alt. 633 m; on log of *Albizia lebbeck* (L.) Benth.; 27.VIII.2016, Gore Vijay (GVU/MVP-289) • Marathwada, Aurangabad district, Taluka Sillod, Palshi; 20°16′56″N, 075°34′15″E; alt. 629 m; on log *Ficus racemosa* L.; 31.X.2019; Gore Vijay (GVM-754) • *ibid.*; Taluka Soygoan, Hadas Kankarada; 20°35′45″N, 075°35′03″E; alt. 333 m; on log of *Vachellia nilotica* (L.) P.J.H. Hurter & Mabb. 09.XI.2019; Gore Vijay (GVM-787) – **Jharkhand** • Sahibganj district, Mandro Block, on the forest way to Chaldhi from Chota Solbandha; 25°12'40″N, 087°36'30″E; alt. 229 m; on dead branches of *Morus alba* L.; 18.VIII.2013; ME Hembrom (MEH-13-008) – **Bihar** • West Champaran district, Valmiki National Park; 27°26′22.7″N, 083°56′39″E; alt. 137 m; on dead branches of *Shorea robusta* Gaertn. 11.X.2019; ME Hembrom (MEH-19-15).

Identification. Basidiomata annual, solitary to caespitose or in groups, leathery when fresh, brittle when dried, substipitate to almost pileate with tapered base, easily separable from host wood. Pileus 34–62 × 24–46 mm, semicircular to more or less spathulate, reflecting the pores below (tessellate), pilear surface smooth, weakly zonate, weakly striate, sulcate near base in some specimens, creamy white to yellowish white to pale yellow (4A2–3) when young turning ochraceous with maturity, gradually darkening towards margin. Margin sterile, entire to lobed in some specimens, acute, inrolled when dried, pale orange to light orange (5A3–5) when young, drying brownish orange to dark brown (5F6–8). Hymenophore poroid, hexagonal/radially elongated, 0.5–7 × 0.5–3 mm, yellowish white to pale yellow (3A2–3) when young turning pale orange with maturity (5A3). Context to 3 mm thick in pilear region, gradually widening towards base, homogenous, cream colored. Tubes 1–6 mm long, shallow near margin and base, dissepiments thin, entire to more or less lacerate with maturity, orange to deep orange (5A6–8) when young turning golden yellow (5B7–8) with maturity. Stipe 3–7 × 2–3 mm, lateral, glandular, smooth, concolorous with pilear surface (5A3).

Pileipellis undifferentiated, composed of non-agglutinated dense hyphae. Context composed of loosely interwoven with dominating skeleton-binding hyphae, generative hyphae rare; generative hyphae 1.5–2.0 µm wide, rare, clamped, smooth, thin-walled, smooth, hyaline; skeleto-binding hyphae 2–6 µm wide, moderately to thick-walled wall to 2.5 µm thick, frequently branched, smooth, hyaline. Trama composed of loosely interwoven with dominating skeleto-binding hyphae, generative hyphae rare; generative hyphae 2–5 µm wide, rare, clamped, thin-walled, branched, smooth, hyaline; skeleto-binding hyphae 2–6 µm wide, moderately to thick-walled wall up to 2.5 µm thick, frequently branched, smooth, hyaline. Hymenium composed of basidia, basidioles, and cystidioles; cystidioles 11–33 × 6–12 µm, infrequent, thin-walled, smooth hyaline. Basidia 23–28 × 7–9 µm, clamped at base, thin-walled, smooth hyaline,

Figure 3. *Favolus roseus*. **A.** Habitat. **B–D.** Habit showing macromorphological features. **E.** undifferentiated pileipellis composed of non-agglutinated dense hyphae. **F.** Basidia (white arrow) and cystidioles (black arrow). **G.** Basidiospores. Scale bars =10 µm.

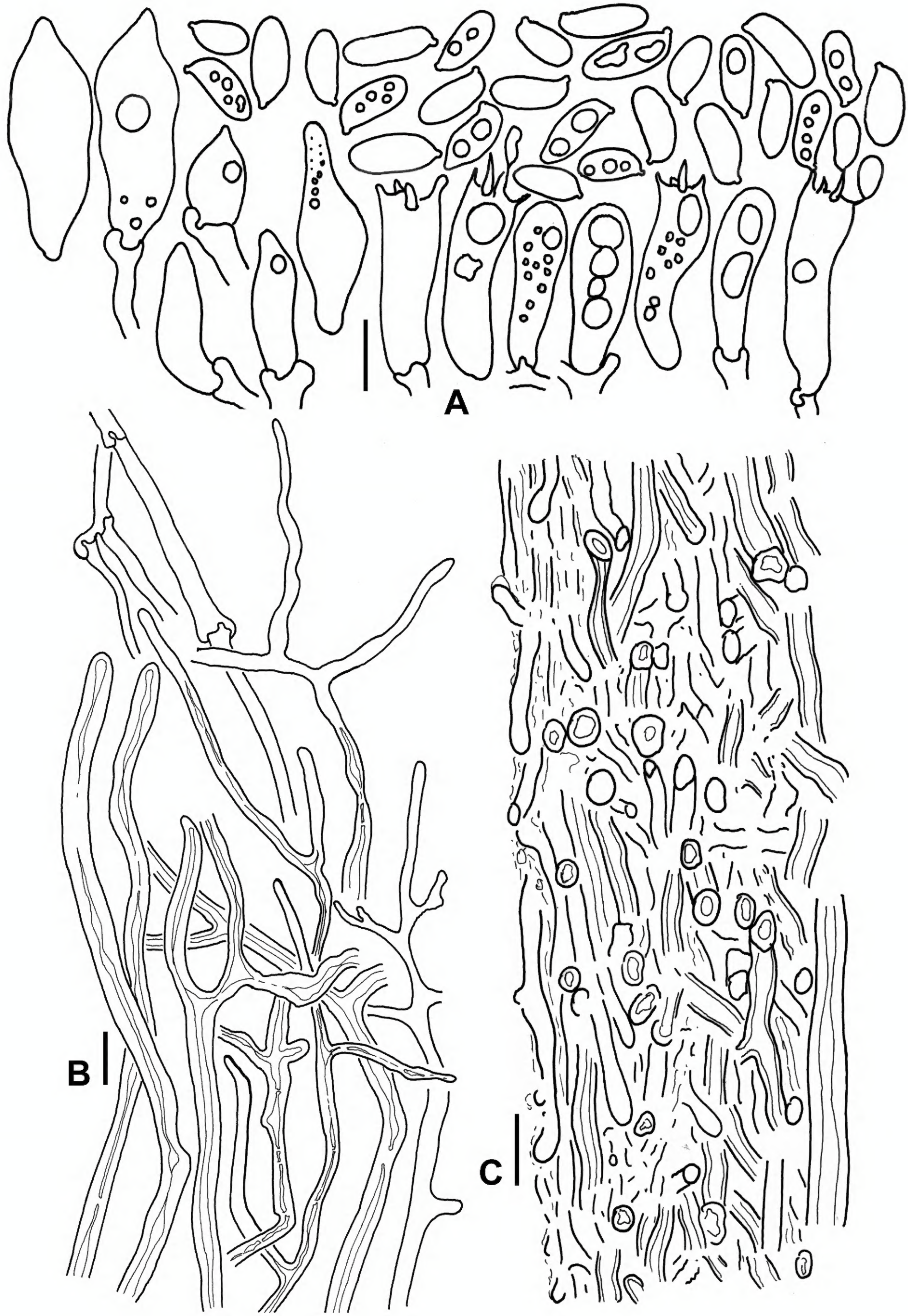

Figure 4. *Favolus roseus*. **A.** Basidia, Basidioles, Cystidioles and Basidiospores. **B.** Generative and skeleto-binding hyphae. **C.** Drawing showing undifferentiated pileipellis composed of non-agglutinated dense hyphae. Scale bars =10 µm.

4-sterigmate (sterigmata 1.5–4 µm long). Basidiospores 8.0–(11.01)–12.9 × 3.1–(4.13)–5.1 µm, Q = 2–(2.51)–3.28 (n = 70), cylindrical, thin-walled, smooth, apiculate, hyaline, non-amyloid.

Discussion

We sampled from large areas of India covering the three large states of Bihar, Jharkhand and Maharashtra in order to record the morphological features and our data were similar to that of Sotome et al. (2013). Until now, wood-decaying polypores in India have seldom been phylogenetically compared with well-known taxa elsewhere in the world, and thus, we phylogenetically compared Indian *F. roseus* with materials from Tanzania, Sri Lanka, Singapore, and Malaysia. Our phylogenetic analysis using combined nrITS and nrLSU genes resolved both *Favolus* and *Neofavolus* as separate monophyletic groups with significant support (MLBS = 90%). Our multigene phylogenetic results shows that our Indian *F. roseus* (GVM-754, GVM-758 and MEH-19-15) are nested within the *F. roseus* clade (Fig. 1, blue arrow) consisting of Sri Lankan, Malaysian, and Tanzanian specimens (UOC WASNP W13, TFM F-20589, and IJ04, respectively) with strong bootstrap support (MLBS = 100%). This suggests a strong similarity or conspecificity of Asian and African *F. roseus*. In addition to our phylogenetic analysis, a comparison of morphological characters of *F. roseus* and related species in Southeast Asia are presented in Table 2.

The following specific epithets are used for Indian *Favolus*: *F. brasiliensis* (Fr.) Fr., *F. bengala* Bose, *F. boucheanus* Klotzsch, *F. grammocephalus* (Berk.) Imazeki, *F. jacobaeus* Sacc. & Berl., *F. spatulatus* (Jungh.) Lév., *F. tenerrimus* Berk., *F. tenuiculus* P. Beauv., and *F. tessellatus* Mont. (Bakshi 1971; Bilgrami et al. 1991; Roy and De 1996; Leelavathy and Ganesh 2000; Mohanan 2011; Sharma 2012). Among these names, *F. boucheanus* and *F. spatulatus* are now placed in the genus *Polyporus* P. Micheli ex Adans. and *Royoporus* A.B. De, respectively, and *F. jacobaeus* and *F. tenerrimus* are without any clear taxonomic placement (as per Species Fungorum 2021). The taxonomy of *F. brasiliensis*, *F. tessellates*, and *F. roseus* is controversial, as these are treated by some authors as synonyms of *F. tenuiculus* (Species Fungorum 2021), whereas, *F. brasiliensis* and *F. roseus* are cryptic species behind the *F. tenuiculus* (Sotome et al. 2013). However, the combination of morphological features, such as small basidiomata (34–62 × 24–46 mm) with greyish orange to yellowish orange pileus surface (undifferentiated pileipellis composed of non-agglutinated dense hyphae), radially elongated large pores (1.0–4.0 × 0.5–1.5 mm) and basidiospore size (8.0–12.9 × 3.1–5.1 µm), suggest that our material belongs to *F. roseus*, as circumscribed by Sotome et al. (2013).

Favolus grammocephalus is easily morphologically differentiaed from *F. roseus*, including our Indian specimens, due to its small pores (3–5 per mm; Sharma 2012). *Favolus brasilensis* (basidiospores 9–12 × 2–3 µm; Sharma 2012) and *F. spatulatus* (basidiospores 5–8 × 2–3 µm; De 1996) have a white pilear surface when fresh, coupled with a narrower tube (2 mm; Sharma 2012), which is in contrast to the yellowish-white to pale-yellow pilear surface and wider tubes (to 6 mm) in *F. roseus*. But, the name *P. tenuiculus* (although its identity was questioned by Sotome et al. (2013) has been applied several times for specimens having white pileus with short distinct stipe, decurrent hymenophore, presence of gloeoporus hyphae and cystidioles (Roy and De 1996; Leelavathy and Ganesh 2000; Mohanan 2011; Sharma 2012). All of these three taxa are part of *F. tenuiculus* species complex which look superficially alike, but their pilear surface micromorphology and phylogeny reveals them to be independent taxa, of which *F. roseus* was unknown from Indian mycobiota.

Extralimital species like *F. septatus* J.L. Zhou & B.K. Cui is a similar species reported from south China. It has a pinkish-buff to yellowish-brown pileus and yellowish-brown to apricot-orange hymenophore, but its pores are smaller (0.5–1 per mm) and its stipe is short but distinct (Zhou and Cui 2017). The temperate North American *Neofavolus americanus* J.H. Xing, J.L. Zhou & B.K. Cui macromorphologically looks similar to *F. roeseus* but is distinguished by its glabrous pilear surface with pileipellis as a cutis composed of parallel and agglutinated generative hyphae (Sotome et al. 2013). *Neofavolus* is also restricted to the northern temperate region (Sotome et al. 2013).

Our study partially resolves the taxonomy of the *F. tenuiculus* complex from India using molecular tools. Future phylogenetic studies will likely find additional hidden diversity in the genus *Favolus*, including in the *F. tenuiculus* species complex.

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Authors' Contributions

Conceptualization: AG, MEH. Data curation: AG, VUG, VPM. Formal analysis: AG, MEH. Investigation: VUG, MEH, VPM. Methodology: VPM. Resources: AG. Writing – original draft: AG, MEH. Writing – review and editing: AVK.

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Table 2. Morphological characters comparison of *Favolus roseus* and related species in Southeast Asia (after Roy and De 1996; Sharma 2012; Sotome et al. 2013; Zhou and Cui 2017).

Name of the taxa	Pileus and Pilear surface	Pores	Pileipellis	Skeletal-Binding hyphae	Generative hyphae	Gloeoporus hyphae	Cystidioles	Basidiospores
F. roseus	Reflecting the pores below (tessellate), faintly striate with radial lines, yellowish orange when fresh	1–3 × 0.5–2 mm, radially elongated, yellowish orange to brownish orange	Not well differentiated	3–6 µm wide, thick-walled, moderately branched	Up to 5 µm wide, clamped, thin-walled	Not mentioned	Not mentioned	7–12 × 2.4–4.2 µm, cylindrical
F. roseus (present study)	Reflecting the pores below (tessellate), weakly striate, creamy white to yellowish white to pale yellow becoming ochraceous	0.5–7 × 0.5–3 mm, hexagonal/radially elongated, yellowish white to pale yellow becoming pale orange	Not well differentiated	2–6 µm wide, thick-walled, frequently branched	1.5–5 µm wide, clamped, thin-walled	Absent	11–33 × 6–12 µm	8–12.9 × 3.1–5.1 µm, cylindrical
F. brasiliensis	Reflecting the pores below (tessellate), radially striate to almost smooth, white when fresh drying cream to brownish orange	2–4 × 1–2 mm to (1–3 per mm in Indian materials), radially elongated, white when young	Not well differentiated	3–7 µm wide, thick-walled to solid, somewhat tortuous, rarely to moderately branched	2–3.5 µm wide, septate, thin-walled	Not mentioned	Absent	7–12× 2.2–4.6 µm, cylindrical
F. emerici *	Non-tessellate, partly scrupose or spinulose near base, strongly radially striate, orange to reddish brown	3–5 per mm, round to angular, white when young becoming cream to orange	Well differentiated, 10–35 µm wide, composed of densely arranged parallel hyphae	3–4.5 µm wide, thick-walled to solid, bovista type, frequently branched (5–7.5 µm wide in Indian material)	2–5 µm wide, clamped, thin to occasionally slightly thick-walled	Not mentioned	20–24 × 5–6.4 µm	8.1–12 × 2.7–4.8 µm, cylindrical (5–7.5 × 2.4–3.2 µm, ellipsoid cylindrical in Indian materials)
F. septatus	Tessellate nature not mentioned, glabrous, without radial striate, pinkish buff to yellowish brown	0.5–1 per mm, radially elongated, yellowish brown to apricot orange when dried	Not mentioned	1.5–6.5 µm wide, rarely inflated up to 10 µm, thick-walled and septate, arboriform type, infrequently to frequently branched	1.5–6.5 µm wide, clamped, thin-walled	Not mentioned	Absent	7.5–10 × 3–4 µm, cylindrical, rarely oblong
F. spatulatus	Reflecting the pores below (tessellate), strongly radially striate, white when fresh drying fulvous to umber to straw to reddish brown	Up to 1.5 × 0.5 mm, (1–4 per mm in Indian materials), radially elongated, concolorous with pilear surface	Not well differentiated	2–6 µm wide, unbranched and flexuous to occasionally to moderately branched	Up to 3 µm wide, septate, thin walled	Not mentioned	Not mentioned	5.5–8.7 × 2–3.5 µm, cylindrical
F. tenuiculus	Reflecting the pores below (tessellate), glabrous, smooth, without radial striate, white pinkish buff on drying	1–2 mm wide, hexagonal/radially elongated, concolorous with pileus surface	Not mentioned	4–8.5 µm wide, somewhat tortuous, irregularly wide, thick-walled to solid, similar to skeletal hyphae, rare to moderately branched	3.3–5 µm wide, clamped, thin to moderately thick-walled	Up to 8.5 µm wide, clamped, thin walled	15–20 × 3–4 µm	8.3–12 × 2.5–4 µm, ellipsoid cylindrical

**F. emerici* = *Polyporus grammocephalus* Berk. (Roy and De 1996; Sharma 2012).

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